

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

On protein - protein search, using sw model

Run on: August 19, 2003, 15:17:50 ; Search time 43 Seconds
(without alignments)

Sequence: 1 MKTRTFPNKLNTLNTQRLS.....LAGISLGLTWGIFTIRTRKHD 757
1693.016 Million cell updates/sec

Title: US-09-494-297-2
Perfect score: 3945
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 7.6:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO. Score Query Match Length DB ID Description

ALLIGMENTS

RESULT 1
S40043
adhesin - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Accession: S40043
R;Sela, S.; Aviv, A.; Tovi, A.; Burstein, I.; Caparon, G.; Hanski, E.
Mol. Microbiol. 10, 1049-1055, 1993
A;Title: Protein F, an adhesin of Streptococcus pyogenes binds fibronectin via two di
A;Reference number: S40043; MUID: 95020565; PMID: 7934855
A;Accession: S40043
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-659 <SEL>
A;Cross-references: GB:L10919; NID:9425479; PIDN:AAA26964.1; PID:9425480

Query Match 16.1%; Score 633.5; DB 2; Length 659;
Best local Similarity 26.1%; Pred. No. 9e-30; Mismatches 203; Conservative 128; Predicates 237; Indels 211; Gaps 30; Matches 203;

QY 20 SKNSKRENTVLYGVLFMLALVTSVQAKTVGLVLSSTPNAINPSSSEPRWYQESVV 79
Db 24 TKKRKFPAVTLYGVFFMLACAGAIGFCQVAADEKTVPHSSP-NPEFPWYDAYG 81
QY 80 RGHPIYKQFRAVDLDRNLEGSRSYQYCFCNUKKAFPLGLGSDSVKKYKHDGISTKFED 139
Db 82 KEPPGYNWTRHDLYNNGRSYQYCFCNTSINPSQSKFETIKMFKLEGNSFVD 141
QY 140 YAMSPRTGDELNQKLRAVMYNGHQNANGTMELGRLENATRVTQEAWVWYSDNAPTSN 199
Db 142 YAHTKLKGKEELQRLLSLLYNNAVPNDANGYMGKGLERLNATIVTOVAVWHTSDNSQF- 200
QY 200 DESFKRSESNLYTSOLSLMSQAKOLIDPLNPLATKPKQPKQVDDFOLISFEDSKDYN 259
Db 201 ETIWESEAKEGKTSRSCVTLMREALKKLIDPMLATAVNK1PSGYRLNIFSE- 254
QY 260 KQYQNLISGGGLYPTKPTPGDPMPMPQNPQQTISVLSRKYAIGDYSKLEGATL---QLT 315
Db 255 EAYGPNLISAEYVPPDPKPGE--TSEINPKPE-----LDPGPIPEDPKH 298
QY 316 GDNVNSFQARVFSSNDIGERIFLSDGTYTLELNSPAGYSTAEPITFKEAGKVYTDG 375
Db 299 DQNLLEPLPPLPVMD---GEEV-----PEVPSSELEPALPPLMPE-----LDG 337
QY 435 PDSEGGKTMPPDFITGEVKY-THIAGRDLFKVTPRDPDTPDTFLKHKKVIEKOREK 493
Db 365 IAGE-----SGETEITEVGQN---QNPVFDIK-----KLPNFGF-S 399

30 139 3.5 1433 1 A36734
31 139 3.5 2366 2 S10317
32 138.5 3.5 625 2 T26215
33 138.5 3.5 1582 2 AC1153
34 138.5 3.5 1983 2 G86643
35 138.5 3.5 2013 2 A11489
36 138.5 3.5 2484 2 T26216
37 138.5 3.5 2607 2 T26215
38 137 3.5 1177 2 I64233
39 135.5 3.4 3283 2 AC1018
40 135 3.4 926 2 D88897
41 135 3.4 1117 2 S23851
42 135 3.4 1176 2 A38056
43 135 3.4 1228 2 I104668
44 135 3.4 1272 2 C90593
45 135 3.4 1301 2 S51323
bacillopeptidase F
toxin B - Clostrid
surface lipoprotein
adhesin homolog Im
hypothetical protein
probable peptidol
hypothetical prote
hypothetical prote
large repetitive p
hypothetical prote
fibronectin-bindin
hypothetical prote
surface-layer 155K
hypothetical prote
surface layer prot
chaperone and heat
SAC3 protein - yea

QY 494 GOATFYSGLTETQFRAATOLAIYFTDSAEALDKDKLKDYGIG-----FG 536

Db 400 GMVYTEDTKEPEVLMGGQ-----SESVFTKDTQTMGSGOTTHQVETDTKEPEVLMG 453

Db 537 DMNDSTLAVAKILVYEAQDS-----NPRQLTDIDFFPNNNKQSLIGTQWHFBDLV 589

Db 454 GQBSR-----VFETKTMQTMGSGOTQIPEIDEDTKEE----- 486

QY 590 TIRMEDKKEVIPVHNLTRKTVTGLAGDRTKDFHFEIELKNNKG-ELL-----SOTVKT 644

Db 487 -VLMGGQSESVFT-----KDTQTMGSGOTP-----QVETDTKEPEVLMGGQSESVFT 536

QY 645 KTNIEFKDOKATINHKHGSLTLLQGLPEGSYLVEKTDSEGGYKVKVNSQEVANATVSKTG 704

Db 537 KDTQTMGSGOTPQIPEIDEDTKEPEVLMGGQSESVFT-----KDTQTMGSGOTP 587

Db 705 ITSDT-----LAFENNK-----EPVVP-TGVDQKINGYLALIVAGISL 743

Db 588 TVEEDTRPKLUFHDDNNERKEVNEERKPTKNITPLPATGDIENLAFLGILSL 646

RESULT 2

SS4418 fibronectin-binding protein precursor - *Streptococcus pyogenes*

C;Species: *Streptococcus pyogenes*

C;Accession: SS4418; A44792; S2848

R;Talay, S.R.; Valentín-Wiegand, P.; Jerlstrom, P.G.; Timmis, K.N.; Chhatwal, G.S.

A;Title: Fibronectin-binding protein of *Streptococcus pyogenes*: sequence of the binding protein. Immun. 60, 3835-3844, 1992

A;Reference number: A44792; MUID:92363585; PMID:1386839

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 371-638 <FA>

A;Cross-references: EMBL:X67947

A;Note: sequences extracted from NCBI backbone (NCBIN:11014, NCBIPI:11015)

A;Genetics:

C;Keywords: fibronectin binding

F;1-49;Domain: signal sequence #status predicted <SIG>

F;50-638/Product: fibronectin-binding protein #status predicted <MAT>

Query Match 15.3%; Score 603; DB 2; Length 638; Matches 207; Conservative 118; Mismatches 248; Indels 182; Gaps 32;

Best Local Similarity 27.4%; Pred. No. 5.5e-28;

Query Match 15.3%; Score 603; DB 2; Length 638; Matches 207; Conservative 118; Mismatches 248; Indels 182; Gaps 32;

Best Local Similarity 19.7%; Pred. No. 0.13; Matches 171; Conservative 124; Mismatches 279; Indels 296; Gaps 46;

Query Match 15.3%; Score 603; DB 2; Length 638; Matches 207; Conservative 118; Mismatches 248; Indels 182; Gaps 32;

Best Local Similarity 19.7%; Pred. No. 0.13; Matches 171; Conservative 124; Mismatches 279; Indels 296; Gaps 46;

Db 313 QLTGDNVNSFQARVFFSSNDIGERIELSDCQTYTTELNSAGYSAEPTFFKVEAGKVVIT 372

Db 291 QRPNESELPEPTLPPV-----MLDG-QEVPEVPSSELEPALRPPMPELQEQEVPEV 338

Db 373 -----IDRQI-EPNKE-----IVEVSYVEANDFEEFSVLITONYAKFYA 414

Db 339 PSESLPEPALPIMPELQEQEVPEVPSVLDIPEDR----- 373

Db 415 KNRNGSSQVYVCNADLKSPPDSIDGGKIMTPDPTGEVKY-THIAGRLFLKVYKPRDT 473

Db 374 -----YEFNNDQSPLAGE-----SGETEYITEVGNG-----QNPVDI 407

Db 474 DPETFLKHKVKEGYREKGQAEYSGITETQIRAAQOLAIYFTDSAKLDRDKLKDHY 533

Db 408 DK-----KLPNETGF--SGNMVETDTKEPGVLMGGQ-----SESVFTKDTOTGS 452

Db 534 GFGDMNDSTLAVAKILVYEAQDSNPP-----QIQLDLPFIPNNKQYSLIGTQWHFEDL 587

Db 453 G-----QTTPQVE-----TEDIKEPGVLMGGQSESVFTKDTOTGMGSGOTQ 501

Db 588 VDI-TRMDKKEVIPVHNLTRKTVTGLAGDRTKDFHFEIELKNNKG-ELL-----QIQLDLPFIPNNKQYSLIGTQWHFEDL 646

Db 502 KEPGVLMGGQSESVFT-----KDTQTMGSGOTP-----QVETDTKEPGVLMGGQSE-- 550

Db 647 NLEF-KDKATINHKHGSLTLLQGLPEGSYLVEKTDSEGGYKVKVNSQEVANATVSKTG 705

Db 551 SVFETKTMQTMGSGOTP-----GPSETVUTIVEDRPKLUFHDDNNERKEPT----- 598

Db 706 TSDETLAFENKKEVVP-TGVDQKINGYLALIV 739

Db 599 -----KNITPLPATGDIENLAFLGILSL 624

RESULT 3

T30856 protein F2 - *Streptococcus pyogenes*

C;Species: *Streptococcus pyogenes*

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000

C;Accession: T30856

R;Jaffe, J.; Natanson-Yaron, S.; Caparon, M.G.; Hanski, E.

Mol. Microbiol. 21, 373-384, 1996

A;Title: Protein F2, a novel fibronectin-binding protein from *Streptococcus pyogenes*

A;Reference number: T220907; MUID:97011581; PMID:8858591

A;Accession: T30856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1039 <FA>

A;Cross-references: EMBL:U031980; NID:91654115; PID:91654116; PIDN: AAC44522.1

C;Genetics:

A;Note: PRF2

Query Match 4.2%; Score 164; DB 2; Length 1039; Matches 171; Conservative 124; Mismatches 279; Indels 296; Gaps 46;

Db 57 STPNAINP-DSSEYRWGYESVYRGHPPYKDFRVAHDLRVLNLEGSRSYQVYCFNLKKAF 115

Db 110 NPLAIGYDKHQLT-TFTNTIAG--LDKQQLSALSFLENKEVLE----- 156

Db 116 PLGSDSSVKKWIKHDGISTKFDYAMSPPRTGDELNOK-LRAVMYHQNANGIMRG 173

Db 157 -----NTNTSDFKSP--IGQQLTYKGVWLYGNGESTKESNYITNG 196

Db 174 L-----EPLNAIRVQEOAVWVYSDNAPIS-----PDESKERESNLVTS 215

Db 197 ISNVGGSIESTY-ETGEFWVWVYVNPNTNPYAVIWLWGFAKRQAGENDNSLVSSA 254

Db 216 QLS-----LMRQALKQLDPNLTAKMP-----KQVPPDF----- 244

Db 255 QIGDYIYEVPHNRYLPTSYGVDISRNK---DIAKLPGOSTGCKNKRUDGEN 310

QY 245 --QISIFESBDKGDKYK -----GYONLILSG-----GLVPTKPT 277
 :
 Db 311 LOGKBEVVKVTKGAKDOSGKELIVOSHLSFNNWGSYKTLRPNSHVSFTNIBALSPSKSG 370
 QY 278 PGDPMPPPNQPOTSVLIRYAIQYISKI -----LEGATIQLCTDNVMSQARFESSID 331
 :
 Db 371 SGTSEF--TKPSITVANKRVAQLPKKKVSDNDVPLPEAFLRSSNGNS-QKLEASNT 427
 QY 332 IGE-RIELSDGTYILTELNSPAGYIA -----EPITF-KVEA 366
 :
 Db 428 OGELIHKDLISGTYOLYETKAPKGQQTWEKLATVYDITTKPAEQMVKRPHSKVKEA 487
 :
 QY 367 GKVYTTID-----GKQIENPNEKEIVEDPYSVEA-----NDFEERFSVLTQNYA 409
 :
 Db 488 NKEVITIVNKHETLIFSGKKIWEDDRDQRQPKIQVOLLNGQKMPNQIC-----VTKNDW 544
 QY 410 KFYV-----AKNNNGSSQVYCFNADIKSPPOSEDGGK -----TMTPDFTGE 452
 :
 Db 545 SYHFKDLPKYDAKNOEYKSV-----AEVKVP---DGKVKSYLGNDIFNRETEFVEEQ 595
 QY 453 VKYTHIAGROLFKVYKPRTDPPFLKHKKVKVKG-----YREKGQAIENSLTEQRLA- 509
 :
 Db 595 NNFNLLEFGWAEIKQSGPKTIDEDLTSGKQKKNIDTAENRQAI-----IVOLYAD 649
 QY 510 -ATOLAIYIFTDGA---ELDKDKLUDYIGFGMDNSTAVAKILVEYAQDSNPNPQLTDL 564
 :
 Db 650 GVAVEGQOTKFISGSNEWSPEFKNUKQYNGT-----NDITSVKEVYVPTSD----- 698
 QY 565 DFFTPNNKVKQSLGTOHWHEDLVDITRMEDKKEVITPV-HNLTRLKTV---TGLAGDRT 620
 :
 Db 699 -----VTKYSAANDIN-----TKREVITQGPNELEETEETPLESGASGGTT 738
 QY 621 KDFHEIE-----LANKNQKLLSOTVKTDK-TNLIFK---DGK---ATINLKH 661
 :
 Db 739 -----TVEDSRPVDTLGSQEQSGDGMWIEEDSATRHKFSKRDIDKGELLAGATMELRD 793
 QY 662 GESLTLOG-----LPEGSYSLVKETDSEGYKV-----KVNSOEVANATVSKT 703
 :
 Db 794 SSGKJISTWISDGQVKDFYLMQPKTE-VETAADAYEATAITPTVNEQ---GQVYNGK 850
 QY 704 GITSDETLAFENKKEPVVPIG---VDQKJ 729
 :
 Db 851 ATKGDAHIVWANDAYKPTKGSGQVIDEELK 880

RESULT 4

AC1533 surface protein (LXGTG motif) [imported] - *Listeria innocua* (strain Clip1262)
 C;Species: *Listeria innocua*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
 C;Accession: AC1533
 R;Glaser, P.; Flangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsilhi, H.; D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001.
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuraphat, G.; Madueno, E.; Maitourham, A.; Maok, C.; Schlieter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species
 A;Reference number: AB1077; MUID:21531279; PMID:1676669

AC1533

QY 10 LNTLNITQVLSKNS-RFTVILVGFMLITAVLTVNGAKTVE-----GLVE----- 55
 :
 Db 330 LSSFDTQKVTMTSERYSLSLTSIDISSEFTNSITEMKLFDDANNLSLIKQKKIKF 389
 QY 56 ---SSTPNAIINFSDSEYR--WYGESYVRGHPYKOFVYAHDLRVNLEGSSRYCFCN 110
 :
 Db 390 YTVATYEKLYNPRAKYNGTW-----TNPRKRTILSDSLMYDGMATMCGYHWS 441
 QY 111 LKKAPFLGSDSS--KKWKKHDGISTKEDYAMSP---RITG---DEUNQKLRAVMY 161
 :
 Db 442 AVNIT-IAIDSTIYSGDDWKAEDNFISATDKDNFLIDFPLVTVTGSVDTTTPGEYITVS 500
 QY 162 GHPQNANGIMGLEPLNAIRVQEAWYQDSNAPSNPDSFSKRESESNLVTSOLSLMR 221
 :
 Db 501 -----VNLGLTITVTVKENQASWAENSTYT-KESWK-AEDNEVSATN--KK 545
 QY 222 QALKQOLIDPNLATKMPKQVDPDFQD-----SIFESDK---GDKY 258
 :
 Db 546 GKIADISSVTVTGEVDVNTPDYELMTIDGVSTKIVTKEDKSSIEAKOSILYGDW 605
 QY 259 NK-----GYONLILSGLVL-----KPPPGDPMPMPNQPOTSVLIRYAIQD 302
 :
 Db 606 NSKDNFTISATDKDGPNVDFKDKIVSCTVNTIKPGTKVTVLYGNGOSKEVITVK---AD 661
 QY 303 YSKLLEGATLQLTGDNVNSIQARVASSNDIGERELSD---GYTLETELNSPAGYSIE 358
 :
 Db 662 QSTLAKDSIIVYQKWNKAONFATDKDQGPNPVFKDIEVEGTVDTT-----K 710
 QY 359 PITFKVEAGKVYTTIDGKQIENPNEI----VEPVYEAVNDFEFSVLTQNYAKFY 413
 :
 Db 711 PCTNKKI-----TVIY-----NLSEVTVVKAQATLE-KDSALVGDWTNSKDNFIS 759
 QY 414 AKNNKGSSQVYCFNADLKSPPDSDGKTMTPDFT-TGEVKYTHIAGRLFKYVKPRD 472
 :
 Db 760 ATDKOG-----TVDFTPKDKIVSCTVNTIKPGTKVTVLYGNGOSKEVITVK----- 805
 QY 838 GNSVSKFDKIVGTVTVDITKAGTKNVTYVQKSVTITVKADQATLE-----AKDSI 890
 :
 Db 473 TDPDFLKHKKVQKGYREKGQALEYSG---LTETQLRATQALIYFFSDAELDKDL 529
 :
 Db 806 ADQTL-----EVAKDSVYTKDWRKAKDNFTSAT-----DKT 837
 QY 530 KDHQFGDMN-----DSTLA-VAKLIVEVQDSNPNPQLT-----DLDFTIPNNKRYQL 577
 :
 Db 891 IYTGKWAED--NFISATDKAGTKIDFKNKNKVEGTI-----DTTKAGNIDTYSYGV 943
 QY 630 -KNNKQELLSOTVKTDKTNLEFKDKSKATINUKHGSLSLLOCPLPGSYLVE---TDS 683
 :
 Db 944 RSTELSKTITVYVKNOVNLEAKDST-----LYEKGKWIAKDNFVSATDK 988
 QY 684 EGYKVVKVNSQEVANA-----TVSKTGISDETAFENNEKEPV 721
 :
 Db 989 DGNTVDFKATEVKGVNTTAKGTVKITYSYAGISKTIVTVLANKOTKIV 1037
 QY S60138 sex factor aggregation protein precursor - *Lactococcus* lactis
 C;Species: *Lactococcus* lactis
 C;Date: 15-Feb-1995 #sequence_revision 01-Mar-1996 #text_change 15-Oct-1999
 C;Accession: S60138; S49417
 R;Godon, J.-J.; Jury, K.; Shearman, C.A.; Gasson, M.J.
 submitted to the EMBL Data Library, December 1993
 A;Description: The *Lactococcus* lactis sex-factor aggregation gene cluA.
 A;Reference number: S60138
 A;Accession: S60138
 A;Molecule type: DNA
 A;Residues: 1-1243 <GOD>
 A;Cross-references: EMBL:U04468; NID:9458233; PID:AAA66196.1; PID:9458234
 R;Godon, J.-J.; Jury, K.; Shearman, C.A.; Gasson, M.J.
 Mol. Microbiol. 12, 655-663, 1994

QY S60138

QY Match 4.1%; Score 161; DB 2; Length 1386;
 Best Local Similarity 19.7%; Pred. No. 0.3;
 Matches 163; Conservative 127; Mismatches 301; Indels 238; Gaps 41;

| RESULT 6 | |
|---|--|
| AB1317 | probable peptidoglycan bound protein (LPXTG motif) lmo2178 [imported] - <i>Listeria monocytogenes</i> |
| A;Title: The <i>Lactococcus lactis</i> sex-factor aggregation gene clua. | C;Species: <i>Listeria monocytogenes</i> |
| A;Reference number: S49417; MUID:95020601; PMID:7934889 | C;Accession: 549417 |
| A;Accession: S49417 | C;Status: nucleic acid sequence not shown |
| A;Molecule type: DNA | C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 |
| A;Residues: 61-61; 482-487; 489-824 <GOW> | C;Genetics: |
| A;Cross-references: EMBL:U04468 | C;Cross-references: |
| A;Gene: clua | C;Gene: |
| F;1-43/Domain: signal sequence #status predicted <SIG> | A;Title: Comparative genomics of <i>Listeria</i> species |
| Query Match 4.0%; Score 159; DB 2; Length 1243; | A;Reference number: AB1077; MUID:21537279; PMID:1679669 |
| Best Local Similarity 19.6%; Pred. No. 0.33; Mismatches 160; Conservative 100; MisMatches 243; Indels 314; Gaps 42; | A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourna, A.; Entian, K.D.; Fsihi, A.; Schlueer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehrl, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, A.; Status: preliminary |
| Matches 160; | A;Molecule type: DNA |
| QY 98 LEGSRRYQWYCFNLKKAFLPLGSDDSVVKWYKKHDGISTKFEDYAMSPRITGDELNQKLRA 157 | A;Residues: 1-612 <GLA> |
| Db 335 MAGSLNYS-----KSKTPPEGGLPPTSDCGYNQHSSVS - FDN-----TL 370 | A;Cross-references: GB:NC_003310; PID:CAD00256.1; PID:g16411648; GSDB:GN00177 |
| QY 158 VMYNGHPONANGIMEGLEPLNATRIVTOEAWYYSNDAPAPISNPDESFKRESESNLVTSOL 217 | A;Experimental source: strain EGD-e |
| Db 371 VWSYFPPSSGVHKVSG-RPTSGANATGDS--WSSNPPSNETWASATAYTDYKAIGPS-- 424 | A;Gene: lmo2178 |
| QY 218 SLMRQALKOLIDDNLATK---MPKQVDDDFQQLS1FSEDESKDGYKYNKGQNL - LSGGL 270 | Query Match 4.0%; Score 159; DB 2; Length 1612; |
| Db 425 -----LDTYTEMQGKTRNWSWYGMMLNIPKDGQTISIVNGTDP---ANMWALLNGQ 471 | Best Local Similarity 20.9%; Pred. No. 0.5; Mismatches 320; Indels 278; Gaps 47; Matches 184; Conservative 99; MisMatches 320; Indels 278; Gaps 47; |
| QY 271 VPTPKPPTPQDPPMPMNPQPTOTSVLIRKVAIGDYSKLLCATOLQTLGDNYNSFQARVEFSSN 330 | Db 825 STKPNL-----WWFY-SYVQWAKVSDNGVG-----EKSYQYQYASKLENAM 867 |
| 472 LPNPKTPP-EPP1PVKPKTATYDQATQDNTK---AVTQDGTDLN----- 516 | QY 116 -----PLGDSVVVKWYKHDGISTKFEDYAMSPRITG 148 |
| 331 DIGERRIELSD-GIVTLEELNSPAGYSIE-----PITFKEAGKVTT-----ID 374 | Db 868 TKTATIDPSFDNKNVNIVTLLNISADPRINPPTIDTMKTTGTAQVWKFVSKFVNNETG 927 |
| QY 517 --GALVNUKQETENWVNLNEVLPAGHEVIKSYVMTDPLPEGFKLDEQSKLNLSPDYLTD 574 | QY 149 DELNQKURAVWYNGHQNANGIMEGLEPLNATRIVTOEAW--WYSDNAISNP----- 200 |
| QY 375 GK-----QIENPKEIVEPVSYVRAINYDPEFSVLTQVAKFYAKNNGSSV 423 | Db 928 EDDISKVYDITYTDN - NFTIOPFKYKATAPAKIVTYSIIMSGLVNTATATSPDYGSL 985 |
| Db 575 EKTNTVTLTAYKATEAMKNDLQNAQYQVPE-----TLCQCV-----TQGSS-- 617 | QY 201 -----ESFKRESEENLVTSQLS1MRQALKQLIDPLATKMPKQVYPDDFOLSI 248 |
| QY 424 VYCNADLKSPPDSEDDGKIMTPDFT--TGEVKYTHIAGRDLFKYTVKPRDTDDEFLKH 481 | Db 986 PMTYKRTTS1SPAFITGSGSGSTATGSLETK---VYKDKNSK - KTGAKTQLYT 1037 |
| Db 618 --FKNDL-----ETLINDYTIVNSNEVE-----VHTPDPKPEKSNEN 651 | QY 249 FESEDKG---DKYVKGQYQULSGG---LVPTRKPPP-----GDP 281 |
| QY 482 IKVKEIKGYREKGQAE-----ISGLTEQO--LRAATOLAIYFTDSA- 522 | Db 1038 LEGDKAQEOATTDSDGKIVMGLQSGKQYKLMETEAPGTTYSDEYKDGKETTVADIAT 1097 |
| Db 652 -----ASGTTINGOGIDVNATNYYKLLWPLSGYKGIASSKEDIVRG-----FYVDAAP 700 | QY 282 PMPMPNQPTOTSVLIRK--YAGDYSKLLCATOLQTLGDNYNSFQANVFSSEDIGEELS 339 |
| QY 523 -----ELDKDKLKDHYG-----FQDMNDSTLAVKILVE----- 551 | Db 1098 VTIENTEOTGSVWLLKEDSATKD--A1AGEFELONADGTRVADLVSND--GKIEVT 1152 |
| Db 701 DVWDVDLKNNISYKDSQGKSVKGITAKVIVSSVKDAPAEVOKVLAQKIAPKQFFFYVDD 760 | QY 340 D---GIVTLEELNSPAGYSIAEPLITFKEAGKVTTIDGKQIENPKEIVEPVSYVAN 396 |
| QY 552 -----YQDSNPPQLT-----DIFFPINNNKQ-----SLI----- 578 | Db 1153 DLAPGQYQFVTFKAPQY-----VLDGA---PKFKEV-----FNO 1185 |
| Db 761 PQTFTYNTVQGTGNVWEIOPMTFKEAGSAGAYQNYDQIDFGNSYEGDTVKNNTIVPKVVK 820 | QY 397 FEEFSVLTTOYAK--FYYAKNKGSSQVYCFNADLKSPPDSEDDGKIMTPDFT-- 450 |
| QY 579 -----GROWH-FDLDVLDIRMEDKEKV1PYTHMLTLRRTVTG----- 614 | Db 1186 -EAATVTKENWAKTGSVWLTKEFEDSVSKATLSGAEEFELQNA-----GTKVRDNLTINAD 1239 |
| Db 821 QVSVDGGKWTWHDSKLDPDTSNQYDQKLPNFTANGDYLTKILLGDNFESSQWTLAKAVT 880 | QY 451 GEVKVHAGLD-FYIVKVR--DIDPTEFLRIKK---VIEKGVEKGOIEVS 500 |
| QY 615 -----LAG-----DRTKDFHFETELKNKNRQELLS1SOTVKUDKTN----- 647 | Db 1240 GKLKEVLDAPDQPKYFETKATGTYELDATPPTFELFQNTAVNVTKENVKTGSTV-- 1296 |
| Db 881 DKLOGNDIAGQFKVLMASQSKDVKDFFNNHVFQDKGKEVQIIFPPDKISDITSLASNDP 940 | QY 501 GLTETOLRAATOLATYFTDSEAELD--KDKLKDHYHGFGDM-----NDSTLAVKILV 550 |
| QY 648 -----LEFKDQKATINLKHGSESLTQLG--PFGSYVLUKEDESEGYKVVKVNSQEVANA 698 | Db 1297 -LTKLDSRSRNLAGAFELQTKLGIVSLKDRWV-BANGQIQLNAPGDQVLFKAP 1354 |
| Db 941 DRLLTLMFKD-----VTKGATGABEANLYL---DREKGKIVAPNIGQL--D 982 | QY 551 EYAQSNPQJLTDIFPNNNKYQ-----SLGQTQWHE-----DLV 588 |
| QY 699 TWSKGTGITSDET--LAFFENKEPVWPTGUDOKINGYL 733 | Db 1355 GYDLDATP-----VEFTIEFNQKAPIOVTKTNTMSTGWSVVLKTGDTGETKALLANATEFKV 1409 |
| Db 983 TWSRT-VTGDNTKOKTCKTNSVNTKIPQDQPTPMNKKV 1018 | |

Db 1410 D---EDNN---VBNLTIDASGKLEITNLAPGDXQLIETKAPAGYELDVPVWKITF 1461
 Qy 632 NKOELLS---QTVKTDKNUNLEFKDGAATNLKHGESLULQGLPPEGYSVLUKEDEG 685
 Db 1462 DOKETLQVTKNLKTVGSKVIAFEVDTKGKV-LAEKEIHT--GI- VGDYKATKADIG 1517
 Qy 686 YKV---KVNSDEVANRATVSKTGITSDETLAFENKKEPV----- 721
 Db 1518 YKLTKOPTNKVGKVFKEKV-----TFVVEKNAPIVNPDKPVTPVKPTKPVPAKK 1571
 Qy 722 -----PTGVYDQKINGYALIJIAGISLGIGIHWIIRK 755
 Db 1572 PTVKTSLSIPTGDESPV---IIFTGLFASFMGLFLIRSK 1608

RESULT 7
 F82884 hypothetical protein uua95 [imported] - Ureaplasma urealyticum
 C;Species: Ureaplasma urealyticum
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: F82884
 R;Glass, J.-I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 A;Submitted to: Genbank, February 2000
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A;Reference number: A82870
 A;Accession: F82884
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5005 <GLA>
 A;Cross-references: PIDN:AAF30907.1; GSPPDB:GN001
 A;Experimental source: serovar 3; biovar 1
 A;Genetics: U0495
 A;Genetic code: SGC3

Query Match 4.0%; Score 157.5; DB 2; Length 5005;
 Best Local Similarity 19.8%; Pred. No. 3.6;
 Matches 158; Conservative 100; Mismatches 285; Indels 253; Gaps 36;
 Qy 5 RFPNKLNTLNFVORVSKNSKRT-----VTL-----VCFVLMIFALVLT 42
 Db 1598 RIKGQNIISITPATISDQDRTYKCMATNLTAGLDYEVSTVPTKQTKNSPITKNS 1657

Qy 43 SMVGAKT---VFGLVESSTFNAINPDSSESYRWRIGYESVVRGHPYKQFRVADLRLVNE 99
 Db 1658 GPGFVTLAPVKLNSM-----DPVHENRNTADIKINLR 1694

Qy 100 GSRSIQCVCNLLKAPPLGDDSSVVKWYK HDGISTKEDYDAMSPTITDELNOKLRV 158
 Db 1695 -IENIGASLNF-----KDIKIFKKKNDGKQISFIHKVTS----- 1728

Qy 159 MYNGHPRONANGIMEGLEPLNAIRVQEAQWVYSDAPISNPDESFKRESNLVTSQLS 218
 Db 1729 -----ANDANEWEKFLDLRNLREYTLERVVY-----LKURDENQNSVNS----- 1768

Qy 219 LMRQALKQLIDPNLATKMPKQVPDFQFOLSLFESEDKGDKYKNGYQNLSSGLVPTK 278
 Db 1769 -----DYLWYIENNLAKTEK-----LLPTKPLGI 1793

Qy 279 GDPPMPNPQQTTSVLLRKVAIGDYSKL EGATIQLTGJDNVNSFQARRFSSNDTGE 334
 Db 1794 IGAPIKEISDNGAKYQKL-KFAINDDVVKENQTFK- NIQPENNNGANLNESEHEG 1849
 Qy 335 RIELSDG-TYLTLELNSPAGYSIAPIRITKEVAGYVTTIDGKQJENPNEKEVE-PYSVE 392
 Db 1850 KVELIDGQKPFVANLNN-----IKVNKEKYVZ-KIYFDEMDQVNGVYKIN 1894
 Qy 393 AYNDEEE-----FSVLTQNYA---KEYVAKNNGSSQVYCFNAIDLKSPPDSEDGK 442
 Db 1895 FKNDYKEPNVWYDASVNTPTVETNKRAIASNNLTDVANKONISINLDS---R 1950
 Qy 443 TMTPDFTTGEVKYTHIAGROLFKYVVKPDTDFLKHITKVKLERYGRQAEYSGL 502

Db 1951 VETIQGHFKAKYISNDNRVWWTNTI-PAPIN-----IGNNNNNAIILNE-L 1995
 Qy 503 TETQL---RAATQOLAIYFTDSAELDKDQLDYHFGDMNDSTLAVAKILVYQADSNPP 559
 Db 1996 NONQLTSNRLYTFALVY--SKDVNE-----NIFANMVYIKNNNPQDSTK 2042
 Qy 560 QLTDDFFIPNNNNKYSLIGTOWHPELDVDTIRMEDKKEVTP-----THNLTTRK 610
 Db 2043 SSTVYDILKAQNADENKITSLLHHSNDQI---FEDKNNHHLKAKISIDELDAHDOINS 2098
 Qy 611 TWIGLAGDRTKFHEELKNNKQELLSQTVTDKNNLEFKGKATINL----- 660
 Db 2099 T-----THDYDTLEKENNEWLKTQTLNL-KPNTKYRKKVWFTSKSDTLYGVN 2149
 Qy 661 -----HGESTLQGLGEGYSVLUKEDEGK-YKVNSQEVANATV-SKQITSD 708
 Db 2150 KDNIVVPIINNNTNDIOLTEKSTLNVKPT---KTNENKNESIKLMLYGENFKNGSSLE 2204
 Qy 709 ETIA---FENNKEPV 720
 Db 2205 NKYAKLUVKDNNNQOI 2220

RESULT 8
 AH1396 peptidoglycan anchored protein (LPXNG motif) [imported] - Listeria monocytogenes (str
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
 C;Accession: AH1396
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguero, F.; Berche, P.; Bloec
 D.; Dominguez-Bernal, G.; Duchaude, B.; Burand, L.; Dussurgey, O.; Entian, K.D.; Fsihi,
 D.; Jones, L.M.; Karst, U.
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Maltournam, A.;
 Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehila
 A;Title: Comparative genomics of *Listeria* species
 A;Reference number: AB1077; MUID:2153729; PMID:1679669
 A;Accession: AH1396
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1530 <GLA>
 A;Cross-references: PIDN:NC_0033210; PIDN:CAD00654.1; PID:916412064; GSPPDB:GN00177
 A;Experimental source: strain EGD-e
 A;Genetics:
 A;Gene: lmo2576

Query Match 4.0%; Score 156; DB 2; Length 1530;
 Best Local Similarity 20.6%; Pred. No. 0.69;
 Matches 160; Conservative 78; Mismatches 221; Indels 316; Gaps 38;
 Qy 193 NAPISNPDESFKR- ESESNLVTSTQSLSMQALKLQDPLNATMPKQVPDFQFOLSLF 250
 Db 794 NMPISPGEYDLTGVDDESN-----LEYFQVKFNEINOSYV-----YQTAITL 839
 Qy 251 SEDK-----GDKYKNGYQNLSSGLVPTK---PPTPGDPPMPNPQNPQPTSVLRYKAI 300
 Db 840 TSDTETTAQIQLNSVTFGDNITKGTEKTEKTMIEVITLGID---GRTGGERGKIIUNLVDK 896
 Db 794 NMPISPGEYDLTGVDDESN-----LEYFQVKFNEINOSYV-----YQTAITL 839
 Qy 301 GDYSKJLEGATLQTLGDNVNSFQARRFSSNDTGE----- 356
 Db 897 ADPSIPLLEGATFDLYA- NDERVDTQTIDKKNVIERDDLVGDTYKEVSAPEGYVLPtas 955
 Qy 357 AEPITPKVE----- 380
 Db 956 TENIQVKLEQDEKVWVOMNEMPIKETGEVHLVKTDKATGATLAGAEFLSYDKSAGELQ 1015
 Qy 381 -----PNKEIV-----EYVSEAYDFE---EYVSEAYDFE---EYVSEAYDFE--- 417
 Db 1016 GLTTDENGELTHNIDGGSVYKLTKEPAGYVQLKSRTWERSVSEQDATEIOAQNEDKL 1075
 Qy 418 ----- 427
 Db 1076 GEAVLTKVDSETNAKLSGAKFNLLNDSGEVQTNJVDENGIEIRVQNLPGDYAQQTEA 1135

Db 1422 DASGNKATQTVNLRLRIVDTSPTLITNNPLTVSIENNRKLTEQELYTAGLIGDNYDIA 1481

Oy 176 PLNAIRTVQEAQWYSSNAPNISNPDESFKR--ESESNLVSQLSLMRQALKQ---- 226

Db 1482 PQQAVQPKQPKVNTSFSTFGDIASVKAQOVOVNLASSG---NQAPQTINN 1537

Oy 227 -----LIDPNLATKMPKQPD 242

Db 1538 VDTVGPKVIAKDNVSYHNTKTEAEFFQDARLVTDDNDDTDLITSNFAEKVNLINKP 1597

Oy 243 DFLQSLTSESEDKGDKYKQGYQNLSSGLVNPKEPTPDRPPMPNQROTTSVLIRKAIGD 302

Db 1598 KVEVITATDIDKGNOTKEITQVQS---KDKPVITADPKI--SYQKIEVTEANFLSGV 1651

Oy 303 YSKLLECATLQLTGDNVNSFQARVFSNDIGERIELD-GTYLTLEINSPAGY-SIAEPI 360

Db 1652 HAEV---TDELGD----VKTSDFAKVKDVKFVKVGTWVLT-LNAKDEBYGNTAEPV 1698

Oy 361 TPKV---EAGKVTIIDGKQIENPKIIVEPVSEANDFREFSVLITONYAKFYAKN 416

Db 1699 KVSVS1FNKLATTFNNADKNTIEAVN---ELPSLESFIKE-----AKDVLGN 1744

Oy 417 KNGSSQVYCFVNADLKSPPDSE-----DGGK----TMTPDFTG-EVKYTHIG 460

Db 1745 K---LKVTTYPHQTKIGNVNPGEISKVTKTQDSGNIAETTVTTLTQKTTGPKMT--- 1797

Oy 461 RDLFKYKWPRTDPDPEFLKKVIEKGYRKGATEYSGLTETQRLAAQALAIY-FT 519

Db 1798 KSTKTKLVEWQSKPWNWTFEGIKATDVGDMYKPNIKDS--EVNLKVKGYPFIFT 1854

Oy 520 DSAELDKKKLKDHYHGGDMNDLSTAVAKLIVYQAQSNPPQITDLEFFIPNNNKYQSLIG 579

Db 1855 DALGNESSESKLAKSTVQITVTSBETLTDKLEISYPGKTI--ISDKQFLQDICTKVNSY 1911

Oy 580 TOWHPEDNDITRMEDKKEVIVTHNIT-----LRKVT---GLAGDRKDHF 624

Db 1912 T-----VKTNTNLKIVDWNKAGCKYKVITVATNSGGVAEKT--- 1948

Oy 625 FEIELKNNQKELSQTVKTDKUNLERK---DGKATINLKHGESLTLQGQIPEGYSYLV 678

Db 1949 ILLTVKNSDSSFLAVPSKDDNNKPKAPNPKGDTLTELIVMMMLLVE--GRMFLR 2005

Oy 679 KETDSEGKVVK 689

Db 2006 RKT----KVK 2011

Oy RESULT 11

S7072 toxin B - Clostridium difficile
C;Species: Clostridium difficile
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 15-Oct-1999
C;Accession: S70172; S44271
R; von Eichel-Streiber, C.; Meyer zu Heringdorf, D.; Habermann, E.; Sartingen, S.
Mol. Microbiol. 17, 313-321, 1995
A;Title: Closing in on the toxic domain through analysis of a variant Clostridium difficile
A;Reference number: S70172; MUID:96079281; PMID:7494480
A;Accession: S70172
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-267 <CON>
A;Cross-references: EMBL:223277; NID:9761713; PIDN:CAA80815.1; PID:9761714
R; Sartingen, S.; von Eichel-Streiber, C.
Submitted to the EMBL Data Library, July 1993
A;Description: Cloning and sequencing of an Clostridium difficile toxin B mutant.
A;Reference number: S44271
A;Accession: S44271

C;Keywords: cytotoxin

Query Match 3.8%; Score 151; DB 2; Length 2367;

Best Local Similarity 19.9%; Pred. No. 2.7; Mismatches 292; Indels 304; Gaps 42;

Matches 171; Conservative 94; Mismatches 292; Indels 304; Gaps 42;

Oy 5 REPNKLNLTQRLV---SKNSKRFVTLVGFVLMFALFTISMGAKTVGLV--SS 57

Db 1568 KFMRKGSNTSDSMLFLESWNKSIIVNFQSONIKFILDANFIISGTTSGFICD 1627

Oy 58 TPWAINGP-----DSSYTRWY-GYESVVRGHPYKQFRAHDLRVNLEGSSYQVCFN 110

Db 111 LKAFAPLGSDSSVKKWVKKHDGISTKFEFYAMSPRITGDEELNOKLRAVVMYHPO---N 166

Oy 1677 FSOQYLGSDCVNK-----VVSPNIXTDEINITPVVETNNTPPEVLD 1722

Db 167 ANGIMEGLEPLNARVQEAQWYSSDNPAPISNPDESKRRESLSNLVTSQSLMRQALKQ 226

Db 1723 ANYTNEKIN-VNINDLSTRYVW-----SNQGND-----ILMSTSEENKVSQKIR 1767

Oy 227 LI---DDNLTAKPKQVFDFFRQDLSLIFSEEDKGD-----KYNQVNLISG- 268

Db 1768 FVWFKDIBTLANKS-----FNSDKDQDVPESEILSFTPSY--YEDGLGYD 1813

Db 269 -GLVPTKPTPGPPMPNPQOPTSVLIRKYAIGDYSKLLCATLQLTGDNVNSQARVE 327

Db 1814 LGLV-----SLYNEKFYINFGFMVSG--LIVINDSLVYFKPV- 1850

Oy 328 SSMDIGERIELSDGTYTTELNSPAGY-SIAEPI-----TPKVEAGKV 370

Db 1851 -NNLITGFTVGSDDKYYENPPINGGA-SIGETIIDDKNYFYNGQVGLQTVFSTEDFKY 1908

Oy 371 -----T-----IDQKQIENPKIETVEP--YSVEAUNDFFSVLTONY-----AKFY 413

Db 1939 FAPANTLDENLEGEAIDFTGKLIDENITYFEDNYRGAWEKLDGEMHVSPETKAFK 1968

Oy 414 AKKRNNGSSQVYCFVNAD--LKSPPDSEDDGKTMPTDPFDTGEVKYTHAGR----- 461

Db 1969 GLNQIGDDK--YYFNSDGMQKGVFSINDNKHFFDDSGVMKVGYTEIDGKHYFAENGEM 2026

Oy 462 -----DLFKYTKPRTDPTDPEFLKKVIEKGYREKGQALEYSGLTETQRLAQL 513

Db 2027 QIGVENTEDGFKY-----FAHNHEDL--GNEGEBSISYGLINLNFKN----- 2066

Oy 514 AIVYFTDSE-----LQDKDLKDYHGFDMN-----DSTIAVAKTLV 550

Db 2067 -IYFDDSFATAVGQWKLDEGSKYFDEDTAERYIGLSLINDQYYFDNDGIMQVGFVII 2125

Oy 551 E-----YAOQSNPQLTLD-----FPIPNNN----- 572

Db 2126 NDKWFYFSDSGTIESGVONIDDDNFYIIDDNGTIVQIGVFTSDGKYFAPANTVNNTYQ 2185

Oy 573 --KQSL-----IGTQHPELDUVDIIMEDKKEVIVPTHNLTRKWTGL 615

Db 2186 AVEYSGLVRVGDVYVYRGTYTTFW-----YDMEONESDKYFVPEH---KACRGK 2236

Oy 616 AGDRTKDHF-----IELKNNQKELSQTVKIDTKNLEFKSGKATINKK--HGE 663

Db 2237 NLIDDIKYFDEKGIMRGLISBENNNYF-----NENGELQGYINIEDKMFVGE 2288

Oy 664 SLLLQ---GLPBGYSYLVKE 680

Db 2289 DGMQIGVFTPDGFKYFAHO 2309

RESULT 12

T28679

fibrinogen-binding protein homolog - Staphylococcus aureus

C;Species: Staphylococcus aureus

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000

C;Accession: T28679

R.; Josefsson, E.; McCrea, K.; Ni, Edhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T.; Microbiology, 144, 3387-3395, 1998
A.; title: Three new members of the serine-aspartate repeat protein multigene family of St A.; reference number: Z20510; MUID:99098700; PMID:9884231
A.; accession: F28679
A.; status: preliminary; translated from GB/EMBL/DBJ
A.; molecule type: DNA
A.; residues: 1-1315 <JOS>
A.; cross-references: EMBL:AJ005646; NID:e1318791; PID:e1318792; PIDN:CAA06651.1
C; genetics: srd

A; Gene: srd

Query Match 3.8%; Score 149; DB 2; Length 1315;
Best Local Similarity 20.2%; Pred. No. 1.4; Matches 203; Conservative 93; Mismatches 336; Indels 372; Gaps 45;
Matches 203; Conservative 93; Mismatches 336; Indels 372; Gaps 45;
Qy 8 NKLWLNITNORVLNSNS- KRFTVTLVGLMFLALVTSANGAKTVFGLWESTP----- 59
Db 208 NSNNNNNAPDILPKSTAPHLNTR----MRIAQNQPSSTEAKVNDLTLTSNTPLTVWDA 262
Qy 60 ---NAINP--DSSSBYRWGYESVURGHYYQFRVAHDLRVNLEGSRSYQVQCFNLKKA 114
Db 263 DKNKIVPQADYLTSKQSTIVDVKVSKGYF-----TIKSYDTWQVGLNPEI 311
Qy 115 FPLOSS---DSSVWKWYKHGD---ISKFDAMSPrTGDILNQKLRAVMNGH-- 163
Db 312 KNIGDIKDPNNGETATAKHDTANNLITYFTDVY----DRFNSVOMGINYNSYMDA 364
Qy 164 ---PQANANGIMEGEPLPNAIRVQEAWMYSDNAPISNPDESFKRESNL----- 211
Db 365 DTIPWSKNUQVEFNVFTIGNTTKFTANIQYDQVYNEKNSIGSAFETYSHVGNKENPGY 424
Qy 212 ----VSTSQLSLMRQALK---QLIDRPLATKPKQFDDFQLSIFESEDKGKYNGY 262
Db 425 KOTIYVNPSSENLSNAKLVQAYHSSYPNIGQINKDWD---IKIYQ-VPKGYTLNGY 480
Qy 263 ONLISGGGLPPIKPPGDPMPMPNQDQPTSVLIRYAGDYSK----- 305
Db 481 D-----WNTKELT-----DVTINQYLOKITYGDNNSAVIDFGNADSAVYVMN 522
Qy 305 -----LLEGATHQLTGD----- 319
Db 523 TKFOITNSSESPTLVQMATLSSIGNKSVSTGNALGFTNNQSGGAGQEVKIRGNYWEDTRK 582
Qy 320 NSFQ-----ARVESSN--DIGRIELSDGTIVTEL-----NSPAGYS 355
Db 583 NGVQELGEKGKVGNVNTVTFDNTNTWKVGAVTKEDGSYLLPQNGDYFVEFSNLPKGVE 642
Qy 355 IAE----- 358
Db 643 VTPSKQGNNEELDSNGLLSSVITVNGKDNISADLGIVKPKYKNGDQYWEITNKGIDQDE 702
Qy 359 -----PTPKVEAGKVY---TIDGK---QIENPNPEI-----VEPYSYEAVNDF 397
Db 703 KGISGVTVILKDENGVNLKTVTIDGAKKTFDLDNGNWKVEFTTPEGITPTVTSID 762
Qy 398 EEFs-VLTQNY-----AKFYYAKNKGSSQVYCFNADLSPPDSD---GKTT 443
Db 763 EKDSNGLATTPGTINGADNMNTLDSGFKYKTPKYNLGNVWHDNTNKDGQ---DSTERKGISGVY 820
Qy 444 MTDFTGTVKSYKHLIAGD-LFVTKVPRDIDPFLKHKKVIERGKRGQALEY-- 499
Db 821 VILKNENGEVQLQPTKTDKGKQFT----- 859
Qy 500 SGLTETOLRATOLAI-VYFTDAELDKK-----LKVY-----IGFG 536
Db 860 SGITPTQVNGSGTDEGIDSANGTSTGTVKIKDNTIDSGFVKPYTINGLGDYVWEDTINKVQ 919
Qy 537 DMDMSTLAVA-----KILVEYAQDSSNPP-QLTDLDFIFINNKQCSLQCTQWHPED 586
Db 920 DKDEKGTSQVTVLKDENDKVLKVTTDNGKQFTDL---NNTYK----- 963
Qy 587 LVDLIRMEDRKKEVLP--VTHNLTLRK---TVTGL--AGDRTKDFHFEIELKNNKQEL 636

RESULT 13
AE1449.

hypothetical protein lin0132 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;accession: AE1449
R.; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science, 294, 849-852, 2001
A.; Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.;
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Solano, J.A.; Voss, H.; Wehla
A.; title: Comparative genomics of *Listeria* species.
A.; reference number: AB1077; MUID:21537279; PMID:11679669
A.; accession: AE1449
A.; status: preliminary
A.; molecule type: DNA
A.; residues: 1-1946 <GLA>
A.; cross-references: GB:AL591022; PID:NCAC95365.1; PID:g16412551; GSPDB:GN00178
A.; experimental source: strain Clip11262
C; genetics:

C;Gene: Lin0132

Query Match 3.8%; Score 149; DB 2; Length 1946;
Best Local Similarity 19.8%; Pred. No. 2.6; Matches 185; Conservative 129; Mismatches 359; Indels 262; Gaps 45;
Matches 185; Conservative 129; Mismatches 359; Indels 262; Gaps 45;
Qy 24 KRFTVTLVGLMFLALVTSANGAKTVFGLWESTP----- 75
Db 63 EKTISDGKEVKPINARTLFLKDGRIQFLGK---SVAIKSASDLMPEMSKTSVTESKY 119
Qy 3 KNILVWIVSVAISAISSAFLTRNDAYAIEFEGFTVSPKGKVLTFFSPDAKNDGAWINN 62
Qy 76 ESYVYRGHPKYKOFRAHDL---RVNLEGSRSYQVYCFNLKRAFFQPLGSDSSY---KKWY 127
Db 120 KATD---TKDKAIAQPKGIVVUKLAEGRYIILDNYALKNKGLNKL-PKNTIVSIDENK 175
Qy 181 -----RVTOEAQWYYSNAPLSNPDESFKRE-SESNLVS--TSQSLMRQALKLDP 230
Db 176 KVLLMGKISTKEDYAMSPRITGDENQKLRAVMNGHPQNANGIMEGLEPLNAT----- 180
Qy 231 -----NL-ATK--MFQVQVDFDOLISFISESEDKGDKYKNC-----GYONL 265
Db 233 KAENRNKATKETTDKTKTDEK---KQEKENNQETKTNTNQATMDNTNKAEGANGS 288
Qy 266 LSGLIVPKRPPCOPD---PMPMPNQPRQTSV---LIRK-----YAIGYSK 305
Db 289 ANGG---DRTGTTKGNANBEGGTKDNQ-NITDVKANEKLTNEAEGLKTFQVPIVVEL 345
Qy 305 LLEG---ATLQIT---GDNVNSFOARVF-SNDIGERTELDG---TYTLTELNSPAGY 354
Db 346 AVEQOKASAKLKLTDESSERLQSLAELYDSENKVKVALSSKANQTFDENSILKYGSEY 405
Qy 355 SIAEPITPKVEASQVYTLIDGKQIENPKKEIVERPYSVAFNDFEEFSVLTTONYAKF--Y 412
Db 406 QVWVQGKYSASDRIQETIFFRVEAKPVVLPKLLERGENYLTAELTATELYKIDEL 465
Qy 413 YAKKNGSSQVWCFNADLKSPPDSED----- 447

Db 466 VLRVKENNSNATSKVVKDANKLTONGKVVKFDSLNSKEYIEMEKLWVGKEVTD 525
 Qy 448 ---FTGGEVK-YTHINGRDLKTYVTPRDT-----DPDFLKHKKV-IEKGYREKG 494
 Db 526 NWYFIASTLKAAPSMAGIDLSYSTEKEGFTAVPINLJTDNSITNRYVAYLEDKANG 585
 Qy 495 QAI-----YSGUTETQRLATOLA-----IYFTDS----- 521
 Db 586 ONAKEVAYSVVNASOKRTAVKVGRTVMDGNYVFTAYISGNNNQSDFTLATPVNAV 645
 Qy 522 -----AELDKKLK-DYHF-----GDMNDSTLAVAKLVEQAQDSNPPQ 560
 Db 646 GLKSKTFVEFSIKEAQRODKLTINYEVFDADWLYDNLTHPLKLYKSDAQCMYDGSVA 705
 Qy 561 LTLDFDFPNNKYYQSLI----- 521
 Db 706 TVDL-----RNKNEITNLLEGGLESETYVYVMTASYNDDGAGIMVDOLIGOSGVFTQK 761
 Qy 598 EVIPVTHNLTRKTVGLAGRTKDFHFEIETKNNKQELLSQTVKT-DKTN-----LEF 650
 Db 762 EIAKVNATFTELESVTINQ-----EVNIKSEAAKLNNSANLKYDKKNNTLVKTVPL 814
 Qy 651 KDGKATNLKHGESLTLQGLPBGSYVLTKETDSEGYKVKVNSQEVANATVSKT---GIT 706
 Db 815 NDDFNKLIMTERGVTVYFEEELAINKEYLVKVED---GLDSGMNQVPGVQLVFKKKASPI 872
 Qy 707 SDETLAFFENRKEPVWPTGVDOKINGLALIVIAGI 741
 Db 873 DKVLLDQOPNK-----LKVGG-----LAGI 892

RESULT 14
 G82875 hypothetical protein UU559 [imported] - Ureaplasma urealyticum
 C;Species: Ureaplasma urealyticum
 C;Accession: G82875
 C;Date: 10-Aug-2000 #sequence_revision 20-Aug-2000
 C;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 A;description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor reference sequence.
 A;Accession: G82875
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1883 <GLA>
 A;Cross-references: GB:AB002154; GB:AF222894; NID:96899557; PIDN:AAF30971.1; GSPDB:GN001
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:
 A;Gene: UU558
 A;Genetic code: SGC3

Query Match 3.8%; Score 148.5; DB 2; Length 1883;
 Best Local Similarity 19.1%; Pred. No. 2.7; Mismatches 276; Indels 277; Gaps 34;
 Matches 155; Conservative 102; Mismatches 276; Indels 277; Gaps 34;

Qy 103 SYQYVCENLKKAF--PLGDSVVKVKKHKGISTKEDYAMS----- 143
 Db 951 NFDTSMENLKYTFDHPMFTSNEKRAERIDAMFKYVDPDENISKLDEKANASSVPPY 1010
 Qy 144 -----PRITGDELNQK-----LRAVMYNGHPONANGIMGLEPLINAIRVQEAWWYS 191
 Db 1011 KKLVLSGIIGEIDTINKSFQDFKVALLTQYNAKINDNSKEEVSKLDPPEL-----EKKY- 1067
 Qy 1912 DNAPISNPDESFKRESESNLVLTSOISL-----MROAQLQOLIDPNAT 234
 Db 1068 -----DKQDFRFGVKKVNVVAQTFILNFADIGEJGNGNGKYFVKPKEKEDYQNLRT 1119
 Qy 235 KMKPQVDP-----DFOQSFESEDKGDKYNGY 262
 Db 1120 KTKYESVSIIGIRPSYLTQNKTYSBOLFKSMINLNEFGTIKLIVDRGDKDNKHLK 1179
 Qy 263 QNLSSGGLVPKPTGDPMPNQDQTTSVLRKAIG-DYKLLEGATIQLTGDWNNS 321

Db 1180 DELTEKEIYPLMILTPAE-----AQINFYDLKSNNSGFTPLTEN-NG 1222
 Qy 322 FQARVFSNDGIGERIELSDGTYTTELNSPAGYSIARPIFKEVAGKVYTD--GKQI 378
 Db 1223 SKFTYTKPKDIPSIEF-----MSVDPAK-YTIVENALSSSH 1258
 Qy 379 ENPK---ETVEPVSV-----EAYND---PEFSVLT-----QWAKF 411
 Db 1259 ENVRKWDYELKERYDVDFKEENEVIKQEAQVKNLTLREFKQNLGFLFGETESTNDLFK 1318
 Qy 412 YYAKNKNGSSQVY---CFNADIKSPPDSEDGKTMDFTGEVKYTH-TAGRDLFRTV 468
 Db 1319 YKSKDFNPSLEDKYKQVFDGKLGIGYRSFGKMYKERVGSPKGEPLDTYNFGNPQNWKA 1378
 Qy 469 KRDTD---PDPFLKHKKVIEKGYREKG-----GOATEYS-GLT----- 503
 Db 1379 KPNQKNVRTVDSTIKGQOLEIERKHNENTNLNGQLQYARGFTIYDIPGSKDYGWL 1438
 Qy 504 -----EQQLRAATOLATYFTDSAELDKKLKDHYGFGDMNDSTLAVAKLIV-EY 552
 Db 1439 GSFGTISQSEELPNADETEVSSVSDYTLINKRKYQEKINEF-----DYNFIAEVLJDY 1493
 Qy 553 AQ-----DSNPQPLDL-DFFLPNNNQYQSLIGTQWHEDLVDTIRMEDKKEVIP 601
 Db 1494 VQTVFIPSQNEIDNLPNWISGLDFNTGNEYFSGDNITKWN-----ERLIP 1540
 Qy 602 VTHNLTRKTVGLAGRTKDH-----FELELKNK-----QELLSQTVK 642
 Db 1541 VNNFLSVNTSNTIALNTLFATNNYEKIQVLANGQALNVYQKNQOLFDYDLTKPKQELESFNK 1600
 Qy 643 TDKTNLEFKDGKATINLKHGESITLQGLPEGSYVLTKETDSEGYKVKVNSQEVANATVSK 702
 Db 1601 VRESFSLSNANFLALL-TKTHDSDVNLN-NSVFLTRLSPK-----SNSYIGK 1645
 Qy 703 TGTSID-----ETLAFFENKEPV 720
 Db 1646 TRITNNSSFKDRWLRKIDWEIYDDNREPI 1675

RESULT 15
 AF1489 cell wall-associated protein precursor wapa (B. subtilis) homolog lin0454 [imported]
 C;Species: Listeria innocua
 C;Accession: AF1489
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
 C;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloechl, P.; Dominguez-Bernal, G.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Kart, U.; Science, 294, 819-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurakpat, G.; Madiueno, E.; Maitouram, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla, A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:2153729; PMID:11679669
 A;Accession: AF1489
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2167 <GLA>
 A;Cross-references: GB:AL592022; PIDN: CAC95686.1; PID: g16412895; GSPDB: GN00178
 A;Experimental source: strain Clp11262
 C;Genetics:
 A;Gene: lin0454

Query Match 3.7%; Score 147.5; DB 2; Length 2167;
 Best Local Similarity 19.0%; Pred. No. 3.8; Mismatches 179; Conservative 111; Mismatches 319; Indels 331; Gaps 46; Matches 179; Conservative 111; Mismatches 319; Indels 331; Gaps 46;

Qy 47 AKVYFGL-----VESSTNAINPDSSESYRWWGYESVVRGHPYKOF-RVARD--- 93
 Db 562 AGSTFGRLNTRLFRYQAVFPGGSPNSDLVFAVMPIEK-PQAPVAKAVNSHLKETG 619
 Qy 94 -LRVNLLEGAS---RSQYVCFLN-KAFLGSDSSVKKWYKHDGI-STKE---DYAM 142
 Db 620 YVELNWERKSPMADGYKVLFENGKAYEYDVGAET--KWTTONKGIMWPTKEEIAEGYAL 676

QY 143 -----SPRITQDELNOK-----LRAWMYNGHPQNANGIMGLEP----- 176
 Db 677 HHDGKGAEAKDPSPVYUTNSGGNYKERTNYWFRVIAQAGNNNTSVQS-:EPRTPSIE 734
 QY 177 -----LNAIR--VTQEAWVYSDNAPTSNPDESFKRESE-SNL 211
 Db 735 ALNKOLGMDYWTSPVRCGEVNRTNGNLFHERDFNLGRGSPINVNNTFNSODATGI 794
 QY 212 VTSQSLSLRQALQKOLIDNATKMPKQPPDFOLSFSEDEKDKY----- 258
 Db 795 FGKGWTSTFEKLVEEENGNIV----WESDKKHHRFR--KDKYEAFFGTYSEITRN 847
 QY 259 -----NKGYONLLSGCLVPTKPTPGDPPMPPNQDQTSVLIRKVAIGDYSKLE- 308
 Db 848 ADGYLKIEDKSEURFLVGRKSEKDITKNE-----LTYETDGKJTSRLA 895
 QY 309 -GATIQLT--GDNY-----NSFQARVFSSNDIGE--RIEISDGTYT--- 344
 Db 895 SGRTVLTTEGELYKELVQPEDRKISIYNDKQELISSTARGKLYRKYTDGLTSIYD 955
 QY 345 -----LTELMSPAG-----YSIASPITEKVEAGGVTIDGKQJIE 379
 Db 955 PKHTEEKPVETTFAYEEKLTETDPVGRTTSYDKAHQQTTLNEKRTTISYNDAG 1015
 QY 380 NPNEKEIVE-----PYSVEAYNDFEEFESVL-TTONYA-----KFYVAKNKNKNSQVY 425
 Db 1016 NPKKEIVDADGLKLJTTTYTYESNNLNUKEVNPKGQEETVYADAGDNITKATDAGTESVY 1075
 QY 426 CFNADLKSPDPDSEOGGKTMPPDFITGEVITYTHIAGRDLKYTVPRD----TDPDTEFLK 480
 Db 1076 NDNNADVTSSPDTEGRKTTYD-----GADAVSETLATESQVSSVTOYDAGN 1123
 QY 481 HIK-----KVIEKGREKGQAIEYSGLTETOLRA----TOLA--IYFTDSAL 524
 Db 1124 PIRSGELSSGGNLIQNSFEKGAGVSNNWLIQSDAKGSMEDNMQSAGALGSGSGSYKL 1183
 QY 525 DKDLKDYHGFDMN-----DSTLAVA-----KILVEYRQDSNPQLTDID 565
 Db 1184 TSEANSTVKGYSSYTORVUVEPETYTFESAWIKTSGMNTNADALLIGRLQDANAKDVTBAG 1243
 QY 565 F-----FIPNNNNYQSLI-----GTQWHPEDLVDIT 591
 Db 1244 WQSNRATSIKKNGDWVKQQLTFTSKNVRQVLYLDNQPAHKKGKJWY--DNVQEE 1301
 QY 592 RMEDRKKEVTPVTHULTRKTVTGLAGDRKDFHEIELNNKQELSOVVKTDKTNLEEK 651
 Db 1302 KGSVASSYMPVWN-----SEFHNGTLPTGMWRTGNTAL--T 1337
 QY 652 DGKATINLK-H-GESLTL--QGLPEGYSVLUKERTDSEGYKVNSQEAVANATVSKTGITS 707
 Db 1338 QAKVVDNOSHSGDSAVYFERKATSEAYTHIVOD-----VPVNQKEAKALTIS-:ALSK 1388
 QY 703 DTELAFFENKEPVVPTGVIDQKINGYLALIVTAGLISGLIG 747
 Db 1389 SE-----DAKANGSVATM---SNDSYVWG 1409

Search completed: August 19, 2003, 15:22:29
 Job time : 48 secs